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## RAW SEQUENCE LISTING

DATE: 08/26/2004

PATENT APPLICATION: US/10/807,635A

TIME: 11:05:31

Input Set : D:\51158-20011.11 - seq list (txt).txt  
 Output Set: N:\CRF4\08262004\J807635A.raw

3 <110> APPLICANT: Daniel E.H. Afar  
 4       Rene S. Hubert  
 5       Kahan Leong  
 6       Arthur B. Raitano  
 7       Douglas C. Saffran  
 9 <120> TITLE OF INVENTION: NOVEL 13-TRANSMEMBRANE PROTEIN EXPRESSED  
 10      IN PROSTATE CANCER  
 12 <130> FILE REFERENCE: 51158-20011.11  
 14 <140> CURRENT APPLICATION NUMBER: US 10/807,635A  
 15 <141> CURRENT FILING DATE: 2004-03-23  
 17 <150> PRIOR APPLICATION NUMBER: US 10/285,045  
 18 <151> PRIOR FILING DATE: 2002-10-30  
 20 <150> PRIOR APPLICATION NUMBER: US 09/547,789  
 21 <151> PRIOR FILING DATE: 2000-04-12  
 23 <150> PRIOR APPLICATION NUMBER: 60/128,858  
 24 <151> PRIOR FILING DATE: 1999-04-12  
 26 <160> NUMBER OF SEQ ID NOS: 71  
 28 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 30 <210> SEQ ID NO: 1  
 31 <211> LENGTH: 2585  
 32 <212> TYPE: DNA  
 33 <213> ORGANISM: Homo sapiens  
 35 <220> FEATURE:  
 36 <221> NAME/KEY: CDS  
 37 <222> LOCATION: (4)...(2136)  
 39 <400> SEQUENCE: 1  
 40 gcc atg ggg gga aag cag cgg gac gag gat gac gag gcc tac ggg aag                          48  
 41       Met Gly Gly Lys Gln Arg Asp Glu Asp Asp Glu Ala Tyr Gly Lys  
 42       1                       5                       10                       15  
 44 cca gtc aaa tac gac ccc tcc ttt cga ggc ccc atc aag aac aga agc                          96  
 45 Pro Val Lys Tyr Asp Pro Ser Phe Arg Gly Pro Ile Lys Asn Arg Ser  
 46                             20                       25                       30  
 48 tgc aca gat gtc atc tgc tgc gtc ctc ttc ctg ctc att dtg ggt                          144  
 49 Cys Thr Asp Val Ile Cys Cys Val Leu Phe Leu Leu Phe Ile Leu Gly  
 50                             35                       40                       45  
 52 tac atc gtg gtg ggg att gtg gcc tgg ttg tat gga gac ccc cgg caa                          192  
 53 Tyr Ile Val Val Gly Ile Val Ala Trp Leu Tyr Gly Asp Pro Arg Gln  
 54                             50                       55                       60  
 56 gtc ctc tac ccc agg aac tct act qgg gcc tac tgt ggc atg qgg gag                          240  
 57 Val Leu Tyr Pro Arg Asn Ser Thr Gly Ala Tyr Cys Gly Met Gly Glu  
 58                             65                       70                       75  
 60 aac aaa gat aag ccg tat ctc ctg tac ttc aac atc ttc agc tgc atc                          288  
 61 Asn Lys Asp Lys Pro Tyr Leu Leu Tyr Phe Asn Ile Phe Ser Cys Ile

ENTERED

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62	80	85	90	95	
64	ctg tcc agc aac atc atc tca gtt gag aac ggc cta cag tgc ccc				336
65	Leu Ser Ser Asn Ile Ile Ser Val Ala Glu Asn Gly Leu Gln Cys Pro				
66	100	105	110		
68	aca ccc cag gtg tgt gtg tcc tcc tgc ccg gag gac cca tgg act gtg				384
69	Thr Pro Gln Val Cys Val Ser Ser Cys Pro Glu Asp Pro Trp Thr Val				
70	115	120	125		
72	gga aaa aac gag ttc tca cag act gtt ggg gaa gtc ttc tat aca aaa				432
73	Gly Lys Asn Glu Phe Ser Gln Thr Val Gly Glu Val Phe Tyr Thr Lys				
74	130	135	140		
76	aac agg aac ttt tgt ctg cca ggg gta ccc tgg aat atg acg gtg atc				480
77	Asn Arg Asn Phe Cys Leu Pro Gly Val Pro Trp Asn Met Thr Val Ile				
78	145	150	155		
80	aca agc ctg caa cag gaa ctc tgc ccc agt ttc ctc ctc ccc tct gct				528
81	Thr Ser Leu Gln Gln Glu Leu Cys Pro Ser Phe Leu Leu Pro Ser Ala				
82	160	165	170	175	
84	cca gct ctg ggg cgc tgc ttt cca tgg acc aac gtt act cca ccg gcg				576
85	Pro Ala Leu Gly Arg Cys Phe Pro Trp Thr Asn Val Thr Pro Pro Ala				
86	180	185	190		
88	ctc cca ggg atc acc aat gac acc acc ata cag cag ggg atc acg ggt				624
89	Leu Pro Gly Ile Thr Asn Asp Thr Thr Ile Gln Gln Gly Ile Ser Gly				
90	195	200	205		
92	ctt att gac agc ctc aat gcc cga gac atc agt gtt aag atc ttt gaa				672
93	Leu Ile Asp Ser Leu Asn Ala Arg Asp Ile Ser Val Lys Ile Phe Glu				
94	210	215	220		
96	gat ttt gcc cag tcc tgg tat tgg att ctt gtt gcc ctg ggg gtg gct				720
97	Asp Phe Ala Gln Ser Trp Tyr Trp Ile Leu Val Ala Leu Gly Val Ala				
98	225	230	235		
100	ctg gtc ttg agc cta ctg ttt atc ttg ctt ctg cgc ctg gtg gct ggg				768
101	Leu Val Leu Ser Leu Leu Phe Ile Leu Leu Leu Arg Leu Val Ala Gly				
102	240	245	250	255	
104	ccc ctg gtg ctg gtg atc ctg gga gtg ctg ggc gtg ctg gca tac				816
105	Pro Leu Val Leu Val Ile Leu Gly Val Leu Gly Val Leu Ala Tyr				
106	260	265	270		
108	ggc atc tac tac tgc tgg gag gag tac cga gtg ctg cgg gac aag ggc				864
109	Gly Ile Tyr Tyr Cys Trp Glu Glu Tyr Arg Val Leu Arg Asp Lys Gly				
110	275	280	285		
112	gcc tcc atc tcc cag ctg ggt ttc acc acc aac ctc agt gcc tac cag				912
113	Ala Ser Ile Ser Gln Leu Gly Phe Thr Thr Asn Leu Ser Ala Tyr Gln				
114	290	295	300		
116	agc gtg cag gag acc tgg ctg gcc gca ctg atc gtg ttg ggg gtg ctt				960
117	Ser Val Gln Glu Thr Trp Leu Ala Ala Leu Ile Val Leu Ala Val Leu				
118	305	310	315		
120	gaa gcc atc ctg ctg atg ctc atc ttc ctg cgg cag cgg att cgt				1008
121	Glu Ala Ile Leu Leu Leu Met Leu Ile Phe Leu Arg Gln Arg Ile Arg				
122	320	325	330	335	
124	att gcc atc gcc ctc ctg aag gag gcc agc aag gct gtg gga cag atg				1056
125	Ile Ala Ile Ala Leu Leu Lys Glu Ala Ser Lys Ala Val Gly Gln Met				
126	340	345	350		

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128 atg tct acc atg ttc tac cca ctg gtc acc ttt gtc ctc ctc ctc atc	1104
129 Met Ser Thr Met Phe Tyr Pro Leu Val Thr Phe Val Leu Leu Leu Ile	
130 355 360 365	
132 tgc att gcc tac tgg gcc atg act gct ctg tac ctg gct aca tcg ggg	1152
133 Cys Ile Ala Tyr Trp Ala Met Thr Ala Leu Tyr Leu Ala Thr Ser Gly	
134 370 375 380	
136 caa ccc cag tat gtg ctc tgg gca tcc aac atc agc tcc ccc ggc tgt	1200
137 Gln Pro Gln Tyr Val Leu Trp Ala Ser Asn Ile Ser Ser Pro Gly Cys	
138 385 390 395	
140 gag aaa gtg cca ata aat aca tca aac ccc acg gcc cac ctt gtg	1248
141 Glu Lys Val Pro Ile Asn Thr Ser Cys Asn Pro Thr Ala His Leu Val	
142 400 405 410 415	
144 aac tcc tcg tgc cca ggg ctg atg tgc gtc ttc cag ggc tac tca tcc	1296
145 Asn Ser Ser Cys Pro Gly Leu Met Cys Val Phe Gln Gly Tyr Ser Ser	
146 420 425 430	
148 aaa ggc cta atc caa cgt tct gtc ttc aat ctg caa atc tat ggg gtc	1344
149 Lys Gly Leu Ile Gln Arg Ser Val Phe Asn Leu Gln Ile Tyr Gly Val	
150 435 440 445	
152 ctg ggg ctc ttc tgg acc ctt aac tgg gta ctg gcc ctg ggc caa tgc	1392
153 Leu Gly Leu Phe Trp Thr Leu Asn Trp Val Leu Ala Leu Gly Gln Cys	
154 450 455 460	
156 gtc ctc gct gga gcc ttt gcc tcc ttc tac tgg gcc ttc cac aag ccc	1440
157 Val Leu Ala Gly Ala Phe Ala Ser Phe Tyr Trp Ala Phe His Lys Pro	
158 465 470 475	
160 cag gac atc cct acc ttc ccc tta atc tct gcc ttc atc cgc aca ctc	1488
161 Gln Asp Ile Pro Thr Phe Pro Leu Ile Ser Ala Phe Ile Arg Thr Leu	
162 480 485 490 495	
164 cgt tac cac act ggg tca ttg gca ttt gga gcc ctc atc ctg acc ctt	1536
165 Arg Tyr His Thr Gly Ser Leu Ala Phe Gly Ala Leu Ile Leu Thr Leu	
166 500 505 510	
168 gtg cag ata gcc cggt gtc atc ttg gag tat att gac cac aag ctc aga	1584
169 Val Gln Ile Ala Arg Val Ile Leu Glu Tyr Ile Asp His Lys Leu Arg	
170 515 520 525	
172 gga gtg cag aac cct gta gcc cgc tgc atc atg tgc tgt ttc aag tgc	1632
173 Gly Val Gln Asn Pro Val Ala Arg Cys Ile Met Cys Cys Phe Lys Cys	
174 530 535 540	
176 tgc ctc tgg tgt ctg gaa aaa ttt atc aag ttc cta aac cgc aat gca	1680
177 Cys Leu Trp Cys Leu Glu Lys Phe Ile Lys Phe Leu Asn Arg Asn Ala	
178 545 550 555	
180 tac atc atg atc gcc atc tac ggg aag aat ttc tgt gtc tca gcc aaa	1728
181 Tyr Ile Met Ile Ala Ile Tyr Gly Lys Asn Phe Cys Val Ser Ala Lys	
182 560 565 570 575	
184 aat gcg ttc atg cta ctc atg cga aac att gtc agg gtg gtc gtc ctg	1776
185 Asn Ala Phe Met Leu Leu Met Arg Asn Ile Val Arg Val Val Val Leu	
186 580 585 590	
188 gac aaa gtc aca gac ctg ctg ttc ttt ggg aag ctg ctg gtg gtc	1824
189 Asp Lys Val Thr Asp Leu Leu Phe Phe Gly Lys Leu Leu Val Val	
190 595 600 605	
192 gga ggc gtg ggg gtc ctg tcc ttc ttt ttc tcc ggt cgc atc ccg	1872

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193	Gly	Gly	Val	Gly	Val	Leu	Ser	Phe	Phe	Phe	Ser	Gly	Arg	Ile	Pro		
194			610			615						620					
196	ggg	ctg	ggt	aaa	gac	ttt	aag	agc	ccc	cac	ctc	aac	tat	tac	tgg	ctg	1920
197	Gly	Leu	Gly	Lys	Asp	Phe	Lys	Ser	Pro	His	Leu	Asn	Tyr	Tyr	Trp	Leu	
198			625				630					635					
200	ccc	atc	atg	acc	tcc	atc	ctg	ggg	gcc	tat	gtc	atc	gcc	agc	ggc	ttc	1968
201	Pro	Ile	Met	Thr	Ser	Ile	Leu	Gly	Ala	Tyr	Val	Ile	Ala	Ser	Gly	Phe	
202	640			645						650					655		
204	ttc	agc	gtt	ttc	ggc	atg	tgt	gtg	gac	acg	ctc	ttc	ctc	tgc	ttc	ctg	2016
205	Phe	Ser	Val	Phe	Gly	Met	Cys	Val	Asp	Thr	Leu	Phe	Leu	Cys	Phe	Leu	
206			660				665				670						
208	gaa	gac	ctg	gag	cg	aac	aa	ggc	tcc	ctg	gac	cg	ccc	tac	tac	atg	2064
209	Glu	Asp	Leu	Glu	Arg	Asn	Asn	Gly	Ser	Leu	Asp	Arg	Pro	Tyr	Tyr	Met	
210			675				680				685						
212	tcc	aag	agc	ctt	cta	aag	att	ctg	ggc	aag	aag	aa	gag	g	ccc	ccg	2112
213	Ser	Lys	Ser	Leu	Leu	Lys	Ile	Leu	Gly	Lys	Lys	Asn	Glu	Ala	Pro	Pro	
214			690				695					700					
216	gac	aa	aag	aag	agg	aag	aag	tga	cagctccggc	cctgatccag	gactgcaccc						2166
217	Asp	Asn	Lys	Lys	Arg	Lys	Lys	*									
218			705				710										
220	cacccccc	acc	gtccagccat	ccaac	ttc	ac	ttc	ggc	ttt	gtccat	ttt	gtggtaa					2226
221	aaaaagg	ttt	taggc	caggc	ggc	gtgg	gtc	tc	ac	cc	tt	caacactt	tg	agg	gtg		2286
222	aggcggg	ccgg	atcac	ctg	ag	tc	agg	atc	g	ac	cc	tg	cca	acat	gt		2346
223	ccgt	ctctat	taaaaata	aca	aaaatt	atg	cc	gag	atg	gg	tg	g	atg	ca	cc	ag	2406
224	ctact	cgg	ga	ggct	gagg	ca	gg	aga	at	cg	tc	ta	cc	gg	gagg	tg	2466
225	ccg	agat	tcg	gc	gc	tcc	aa	cac	ct	gg	tg	ac	ag	act	cc	aa	2526
226	aca	aa	aaaa	aa	aa	ttt	ttt	ttt	aa	aa	aa	aa	aa	aa	aa	aa	2585
228	<210>	SEQ	ID	NO:	2												
229	<211>	LENGTH:	710														
230	<212>	TYPE:	PRT														
231	<213>	ORGANISM:	Homo sapiens														
233	<400>	SEQUENCE:	2														
234	Met	Gly	Gly	Lys	Gln	Arg	Asp	Glu	Asp	Asp	Glu	Ala	Tyr	Gly	Lys	Pro	
235	1			5			10					15					
236	Val	Lys	Tyr	Asp	Pro	Ser	Phe	Arg	Gly	Pro	Ile	Lys	Asn	Arg	Ser	Cys	
237				20			25				30						
238	Thr	Asp	Val	Ile	Cys	Cys	Val	Leu	Phe	Leu	Leu	Phe	Ile	Leu	Gly	Tyr	
239				35			40				45						
240	Ile	Val	Val	Gly	Ile	Val	Ala	Trp	Leu	Tyr	Gly	Asp	Pro	Arg	Gln	Val	
241				50			55			60							
242	Leu	Tyr	Pro	Arg	Asn	Ser	Thr	Gly	Ala	Tyr	Cys	Gly	Met	Gly	Glu	Asn	
243	65			70			75				80						
244	Lys	Asp	Lys	Pro	Tyr	Leu	Leu	Tyr	Phe	Asn	Ile	Phe	Ser	Cys	Ile	Leu	
245				85			90				95						
246	Ser	Ser	Asn	Ile	Ile	Ser	Val	Ala	Glu	Asn	Gly	Leu	Gln	Cys	Pro	Thr	
247				100			105				110						
248	Pro	Gln	Val	Cys	Val	Ser	Ser	Cys	Pro	Glu	Asp	Pro	Trp	Thr	Val	Gly	
249				115			120				125						
250	Lys	Asn	Glu	Phe	Ser	Gln	Thr	Val	Gly	Glu	Val	Phe	Tyr	Thr	Lys	Asn	

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251	130	135	140
252	Arg Asn Phe Cys Leu Pro Gly Val Pro Trp Asn Met Thr Val Ile Thr		
253	145	150	155
254	Ser Leu Gln Gln Glu Leu Cys Pro Ser Phe Leu Leu Pro Ser Ala Pro		160
255	165	170	175
256	Ala Leu Gly Arg Cys Phe Pro Trp Thr Asn Val Thr Pro Pro Ala Leu		
257	180	185	190
258	Pro Gly Ile Thr Asn Asp Thr Thr Ile Gln Gln Gly Ile Ser Gly Leu		
259	195	200	205
260	Ile Asp Ser Leu Asn Ala Arg Asp Ile Ser Val Lys Ile Phe Glu Asp		
261	210	215	220
262	Phe Ala Gln Ser Trp Tyr Trp Ile Leu Val Ala Leu Gly Val Ala Leu		
263	225	230	235
264	240	245	250
265	Val Leu Ser Leu Leu Phe Ile Leu Leu Leu Arg Leu Val Ala Gly Pro		255
266	260	265	270
267	Leu Val Leu Val Leu Ile Leu Gly Val Leu Gly Val Leu Ala Tyr Gly		
268	275	280	285
269	Ile Tyr Tyr Cys Trp Glu Glu Tyr Arg Val Leu Arg Asp Lys Gly Ala		
270	290	295	300
271	Ser Ile Ser Gln Leu Gly Phe Thr Thr Asn Leu Ser Ala Tyr Gln Ser		
272	295	300	
273	Val Gln Glu Thr Trp Leu Ala Ala Leu Ile Val Leu Ala Val Leu Glu		
274	305	310	315
275	320	325	330
276	335	340	345
277	350	355	360
278	365	370	375
279	380	385	390
280	395	400	405
281	410	415	420
282	425	430	435
283	440	445	450
284	460	465	470
285	475	480	485
286	490	495	500
287	505	510	515
288	520	525	
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**VERIFICATION SUMMARY**

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